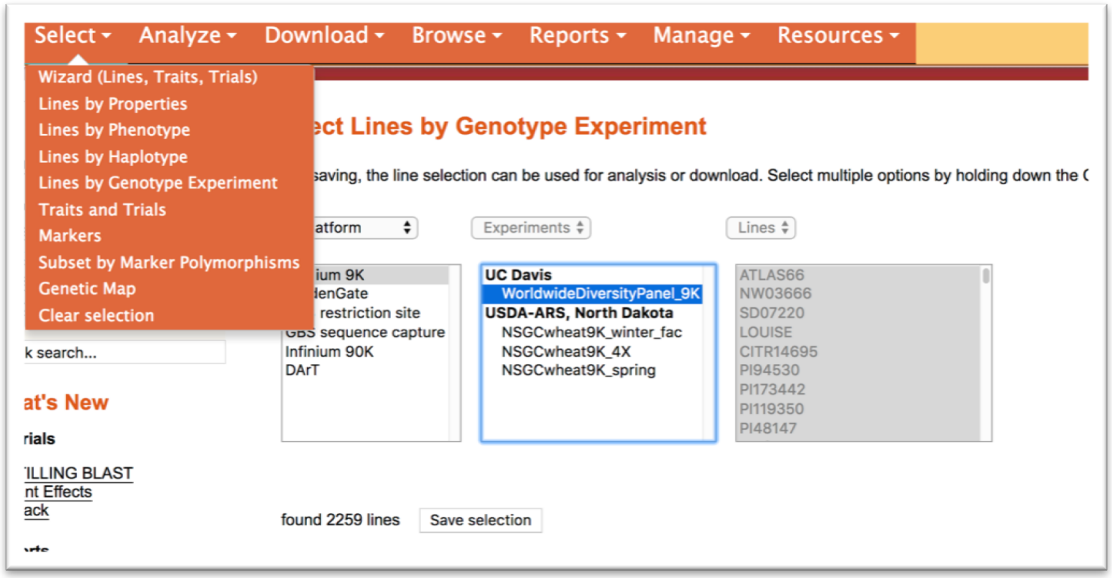
TASSEL is a Java platform for analysis of crop genomic diversity. It provides functionality for association studies, linkage, principal component analysis, cluster analysis, imputation and data visualization. The software is provided by the Buckler Lab for Maize Genetics and Diversity. The program is available from TASSEL Download. Data from T3 website can be accessed by saving from T3 then importing into TASSEL.

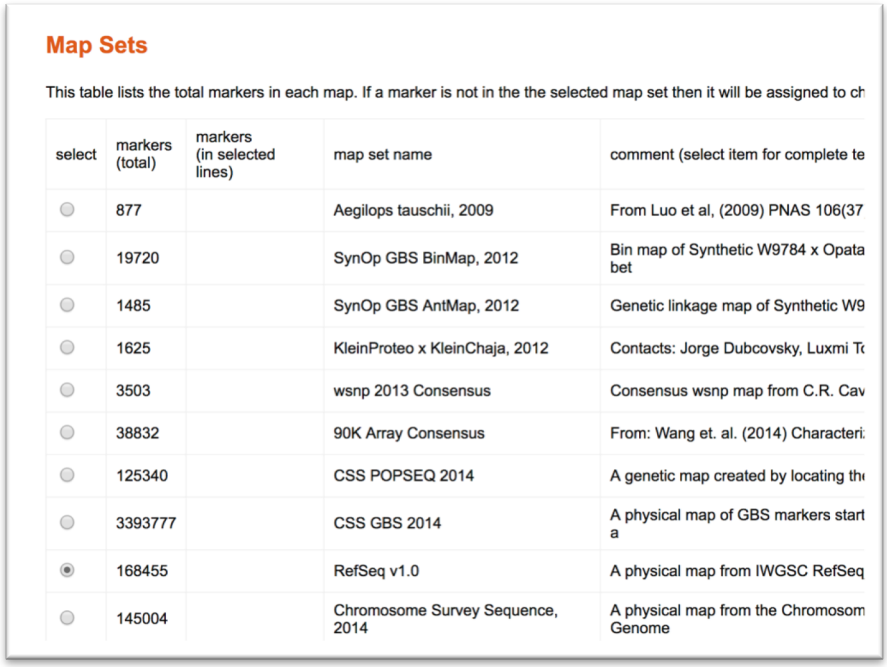
Requirements: TASSEL works with several file formats. The preferred format is VCF because the data from T3 is sorted by position as required by TASSEL. If you use the Hapmap format you may have to sort the data using the tool provided in TASSEL. The "pos" column has to be an integer so values from a genetic map are multiplied by 1000 then converted to integer. If a marker location is not defined in the map then that marker is removed. If two markers are defined at the same location then the duplicate ones are removed.

## Download data from T3 website then import the data into TASSEL

1. The data can be selected by Select => Wizard or Select => Lines by Genotype Experiment



2. Go to Select => Genetic Map

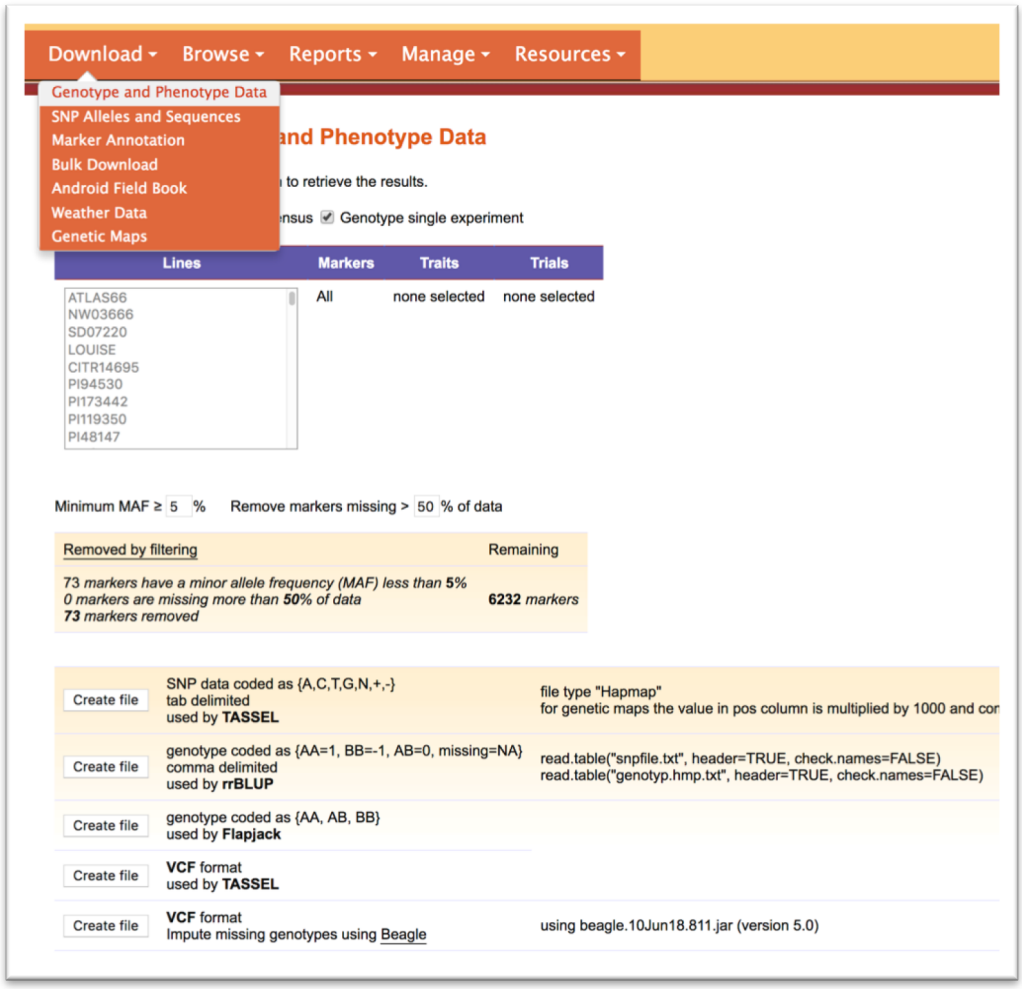


## Map Sets

This table lists the total markers in each map. If a marker is not in the the selected map set then it will be assigned to ch

| select | markers (total) | markers (in selected lines) | map set name | comment (select item for complete te |
|---|---|---|---|---|
| ○ | 877 | | Aegilops tauschii, 2009 | From Luo et al, (2009) PNAS 106(37 |
| ○ | 19720 | | SynOp GBS BinMap, 2012 | Bin map of Synthetic W9784 x Opata bet |
| ○ | 1485 | | SynOp GBS AntMap, 2012 | Genetic linkage map of Synthetic W9 |
| ○ | 1625 | | KleinProteo x KleinChaja, 2012 | Contacts: Jorge Dubcovsky, Luxmi Tc |
| ○ | 3503 | | wsnp 2013 Consensus | Consensus wsnp map from C.R. Cav |
| ○ | 38832 | | 90K Array Consensus | From: Wang et. al. (2014) Characteri: |
| ○ | 125340 | | CSS POPSEQ 2014 | A genetic map created by locating th |
| ○ | 3393777 | | CSS GBS 2014 | A physical map of GBS markers start a |
| ◉ | 168455 | | RefSeq v1.0 | A physical map from IWGSC RefSeq |
| ○ | 145004 | | Chromosome Survey Sequence, 2014 | A physical map from the Chromosom Genome |

3. Go to Download => Genotype and Phenotype Data - Select VCF format
4. Select “Create File”



5. In TASSEL select File => Open then select genotype.vcf file.